SEQUENCE LISTING

<110>   American Home Products

<120>   Aggrecanase Molecules

<130>   GI5435C

<150>   09/---,---
<151>   2001-10-16

<150>   60/241,469
<151>   2000-10-18

<160>   8

<170>   PatentIn version 3.1

<210>   1

<211>   242

<212>   PRT

<213>   Homo sapiens

<400>   1

His Pro Ser Cys Leu Gln Ala Leu Glu Pro Gln Ala Val Ser Ser Tyr
1   5   10   15

Leu Ser Pro Gly Ala Pro Leu Lys Gly Arg Pro Pro Ser Pro Gly Phe
            20   25   30

Gln Arg Gln Arg Gln Arg Gln Arg Arg Ala Ala Gly Gly Ile Leu His
        35   40   45

Leu Glu Leu Leu Val Ala Val Gly Pro Asp Val Phe Gln Ala His Gln
    50   55   60

Glu Asp Thr Glu Arg Tyr Val Leu Thr Asn Leu Asn Ile Gly Ala Glu
65   70   75   80

Leu Leu Arg Asp Pro Ser Leu Gly Ala Gln Phe Arg Val His Leu Val
                85   90   95

Lys Met Val Ile Leu Thr Glu Pro Glu Gly Ala Pro Asn Ile Thr Ala
            100   105   110

Asn Leu Thr Ser Ser Leu Leu Ser Val Cys Gly Trp Ser Gln Thr Ile
            115   120   125

Asn Pro Glu Asp Asp Thr Asp Pro Gly His Ala Asp Leu Val Leu Tyr
        130   135   140

Ile Thr Arg Phe Asp Leu Glu Leu Pro Asp Gly Asn Arg Gln Val Arg
145   150   155   160

Gly Val Thr Gln Leu Gly Gly Ala Cys Ser Pro Thr Trp Ser Cys Leu
            165   170   175

Ile Thr Glu Asp Thr Gly Phe Asp Leu Gly Val Thr Ile Ala His Glu
            180   185   190

Ile Gly His Ser Phe Gly Leu Glu His Asp Gly Ala Pro Gly Ser Gly
            195   200   205

Cys Gly Pro Ser Gly His Val Met Ala Ser Asp Gly Ala Ala Pro Arg
        210   215   220

Ala Gly Leu Ala Trp Ser Pro Cys Ser Arg Arg Gln Leu Leu Ser Leu
225   230   235   240

Leu Arg

<210> 2

<211> 1045

<212> DNA

<213> Homo sapiens

<400> 2
gaattcggcc aaagaggcct acgagtgtgg tcaggatgga gaggtaggac aggaaggagg   60

gctgaatgcg gagtggggac ggacgtccgg agggctggct ggaagctcgc gcgcccctcc   120

-2-

```
cacggggcgg gcgctacctg agcaggctca gcagctgccg gcggctgcag ggggaccagg      180

cgaggccggc gcggggcgcg cgccgtccg aagccatcac gtgtccgctg gggccgcagc       240

cgctgccggg cgcgccgtcg tgctccaggc cgaagctgtg cccaatctca tgggcaatgg      300

tgactcccag gtcgaagcca gtgtcctcgg taatgaggca gctccaggtt ggggagcagg      360

caccgcccag ctgggtgacg ccccgcacct gccggttacc atcaggcaac tccaggtcaa      420

acctagtgat atagaggacc aggtcagcat ggccaggatc cgtgtcgtcc tcagggttga      480

tggtctggct ccacccacag acgctcagca gggacgaggt gaggttggct gtgatatttg      540

gagcaccctc aggctctgtc agaatgacca tcttcaccag gtgcacccga aactgagccc      600

ccagggacgg gtcccgaagc agttctgccc cgatgttgag gttggtgagc acatagcgct      660

ctgtgtcctc ctggtgagcc tggaagacat cggggcccac ggccaccagc agctccaggt      720

gtaggatgcc gcctgcagcc cgcctctgcc tctgcctctg cctctggaag ccaggggaag      780

gagggcggcc ttttaaggga gcaccagggc tcaagtaaga agacacggcc tgtggctcca      840

aagcctgaag acaactcggg tgctacacac acagcggccc cccagttccc ttccggcgtt      900

cgcatctctc atccccatcc cggatcttgg ggaggtcctc ggcttgcccc agtcaaactc      960

gaggttctcc ctatagtgag tcgtattaat ttcagaggag tatttacaag agaagctgaa     1020

gctgtcgaga caaacgaaac tagtg                                           1045
```

<210> 3

<211> 1045

<212> DNA

<213> homo sapiens

<400> 3
```
cactagtttc gtttgtctcg acagcttcag cttctcttct aaatactcct ctgaaattaa       60

tacgactcac tataggagaga acctcgagtt tgactggggc aagccgagga cctccccaag     120

atccgggatg gggatgagag atgcgaacgc cggaagggaa ctggggggcc gctgtgtgtg      180

tagcacccga gttgtcttca ggctttggag ccacaggccg tgtcttctta cttgagccct      240

ggtgctccct taaaaggccg ccctccttcc cctggcttcc agaggcagag gcagaggcag      300

aggcgggctg caggcggcat cctacacctg gagctgctgg tggccgtggg ccccgatgtc      360

ttccaggctc accaggagga cacagagcgc tatgtgctca ccaacctcaa catcggggca      420

gaactgcttc gggacccgtc cctggggggct cagtttcggg tgcacctggt gaagatggtc      480
```

```
attctgacag agcctgaggg tgctccaaat atcacagcca acctcacctc gtccctgctg        540

agcgtctgtg ggtggagcca gaccatcaac cctgaggacg acacggatcc tggccatgct        600

gacctggtcc tctatatcac taggtttgac ctggagttgc ctgatggtaa ccggcaggtg        660

cggggcgtca cccagctggg cggtgcctgc tccccaacct ggagctgcct cattaccgag        720

gacactggct tcgacctggg agtcaccatt gcccatgaga ttgggcacag cttcggcctg        780

gagcacgacg gcgcgcccgg cagcggctgc ggccccagcg acacgtgat ggcttcggac        840

ggcgccgcgc ccgcgccgg cctcgcctgg tccccctgca gccgccggca gctgctgagc        900

ctgctcaggt agcgcccgcc ccgtgggagg ggcgcgcgag cttccagcca gccctccgga        960

cgtccgtccc cactccgcat tcagccctcc ttcctgtcct acctctccat cctgaccaca       1020

ctcgtaggcc tctttggccg aattc                                            1045
```

<210>   4

<211>   2217

<212>   DNA

<213>   homo sapiens

```
<400>    4
cagcttcggc ctggagcacg acggcgcgcc cggcagcggc tgcggcccca gcggacacgt         60

gatggcttcg aacggcgcc gccccgcgcc ggcctcgcct ggtcccctg cagccgccgg        120

cagctgctga gcctgctcag acccgtccct ccgtcgccgc tccctctgct ggccacccac        180

ctctgcgccg gcaggagcct tagtcttggt cccagccaag agccggctcc tggtgggggg        240

cgcgggccga gaactcctgt tcccactcac aaaaggccac gcttccaaac gcttccatcc        300

tcgtgcccac tcctccgtcc cgcctcctcc cggtgtacac cccgggactg agccgggcct        360

gagccgggcc ttgtcgcagc gcatgacggg cgcgctggtg tgggacccgc cgcggcctca        420

acccgggtcc gcggggcacc cgcggaatgc gcacctgggc tctactaca gcgccaacga        480

gcagtgccgc gtggccttcg cccccaaggc tgtcgcctgc accttcgcca gggagcacct        540

ggtgagtctg ccggcggtgg cctgggattg gctgtgaggt ccctccgcat cacccagctc        600

acgtccccc aaacgtgcat ggatatgtgc caggccctct cctgccacac agaccgctg        660

gaccaaagca gctgcagccg cctcctcgtt cctctcctgg atgggacaga atgtggcgtg        720

gagaagtggt gctccaaggg tcgctgccgc tccctggtgg agctgacccc catagcagca        780

gtgcatgggc gctggtctag ctggggtccc cgaagtcctt gctcccgctc ctgcggagga        840
```

```
ggtgtggtca ccaggaggcg gcagtgcaac aaccccagac ctgcctttgg ggggcgtgca      900

tgtgttggtg ctgacctcca ggccgagatg tgcaacactc aggcctgcga gaagacccag      960

ctggagttca tgtcgcaaca gtgcgccagg accgacggcc agccgctgcg ctcctcccct     1020

ggcggcgcct ccttctacca ctgggggtgct gctgtaccac acagccaagg ggatgctctg     1080

tgcagacaca tgtgccgggc cattggcgag agcttcatca tgaagcgtgg agacagcttc     1140

ctcgatggga cccggtgtat gccaagtggc ccccgggagg acgggaccct gagcctgtgt     1200

gtgtcgggca gctgcaggac atttggctgt gatggtagga tggactccca gcaggtatgg     1260

gacaggtgcc aggtgtgtgg tggggacaac agcacgtgca gcccacggaa gggctctttc     1320

acagctggca gagcgagaga atatgtcacg tttctgacag ttacccccaa cctgaccagt     1380

gtctacattg ccaaccacag gcctctcttc acacacttgg cggtgaggat cggagggcgc     1440

tatgtcgtgg ctgggaagat gagcatctcc cctaacacca cctacccctc cctcctggag     1500

gatggtcgtg tcgagtacag agtggccctc accgaggacc ggctgccccg cctggaggag     1560

atccgcatct ggggacccct ccaggaagat gctgacatcc aggtgggagg tgtcagagcc     1620

cagctcatgc acatcagctg gtggagcagg cctggccttg gagaacgaga cctgtgtgcc     1680

aggggcagat ggcctggagg ctccagtgac tgagggggcct ggctccgtag atgagaagct     1740

gcctgcccct gagccctgtg tcgggatgtc atgtcctcca ggctggggcc atctggatgc     1800

cacctctgca ggggagaagg ctccctcccc atggggcagc atcaggacgg gggctcaagc     1860

tgcacacgtg tggacccctg cggcagggtc gtgctccgtc tcctgcgggc gaggtctgat     1920

ggagctgcgt ttcctgtgca tggactctgc cctcagggtg cctgtccagg aagagctgtg     1980

tggcctggca agcaagcctg ggagccggcg ggaggtctgc caggctgtcc cgtgccctgc     2040

tcggtggcag tacaagctgg cggcctgcag cgtgagctgt gggagagggg tcgtgcggag     2100

gatcctgtat tgtgcccggg cccatgggga ggacgatggt gaggagatcc tgttggacac     2160

ccagtgccag gggctgcctc gcccggaacc ccaggaggcc tgcagcctgg agccctg       2217
```

<210> 5

<211> 365

<212> PRT

<213> homo sapiens

<220>

<221> MISC_FEATURE

<223> unknown amino acid

<220>

<221> MISC_FEATURE

<222> (365)..(365)

<223> unknown amino acid

<400> 5

```
Met Asp Met Cys Gln Ala Leu Ser Cys His Thr Asp Pro Leu Asp Gln
1               5                  10                  15


Ser Ser Cys Ser Arg Leu Leu Val Pro Leu Leu Asp Gly Thr Glu Cys
                20                  25                  30


Gly Val Glu Lys Trp Cys Ser Lys Gly Arg Cys Arg Ser Leu Val Glu
            35                  40                  45


Leu Thr Pro Ile Ala Ala Val His Gly Arg Trp Ser Ser Trp Gly Pro
        50                  55                  60


Arg Ser Pro Cys Ser Arg Ser Cys Gly Gly Gly Val Val Thr Arg Arg
65                  70                  75                  80


Arg Gln Cys Asn Asn Pro Arg Pro Ala Phe Gly Gly Arg Ala Cys Val
                85                  90                  95


Gly Ala Asp Leu Gln Ala Glu Met Cys Asn Thr Gln Ala Cys Glu Lys
            100                 105                 110


Thr Gln Leu Glu Phe Met Ser Gln Gln Cys Ala Arg Thr Asp Gly Gln
        115                 120                 125


Pro Leu Arg Ser Ser Pro Gly Gly Ala Ser Phe Tyr His Trp Gly Ala
    130                 135                 140


Ala Val Pro His Ser Gln Gly Asp Ala Leu Cys Arg His Met Cys Arg
145                 150                 155                 160


Ala Ile Gly Glu Ser Phe Ile Met Lys Arg Gly Asp Ser Phe Leu Asp
                165                 170                 175
```

Gly Thr Arg Cys Met Pro Ser Gly Pro Arg Glu Asp Gly Thr Leu Ser
        180   185   190

Leu Cys Val Ser Gly Ser Cys Arg Thr Phe Gly Cys Asp Gly Arg Met
        195   200   205

Asp Ser Gln Gln Val Trp Asp Arg Cys Gln Val Cys Gly Gly Asp Asn
        210   215   220

Ser Thr Cys Ser Pro Arg Lys Gly Ser Phe Thr Ala Gly Arg Ala Arg
225   230   235   240

Glu Tyr Val Thr Phe Leu Thr Val Thr Pro Asn Leu Thr Ser Val Tyr
            245   250   255

Ile Ala Asn His Arg Pro Leu Phe Thr His Leu Ala Val Arg Ile Gly
        260   265   270

Gly Arg Tyr Val Val Ala Gly Lys Met Ser Ile Ser Pro Asn Thr Thr
        275   280   285

Tyr Pro Ser Leu Leu Glu Asp Gly Arg Val Glu Tyr Arg Val Ala Leu
        290   295   300

Thr Glu Asp Arg Leu Pro Arg Leu Glu Glu Ile Arg Ile Trp Gly Pro
305   310   315   320

Leu Gln Glu Asp Ala Asp Ile Gln Val Gly Gly Val Arg Ala Gln Leu
                325   330   335

Met His Ile Ser Trp Trp Ser Arg Pro Gly Leu Gly Glu Arg Asp Leu
            340   345   350

Cys Ala Arg Gly Arg Trp Pro Gly Gly Ser Ser Asp Xaa
            355   360   365

<210>   6

<211>   738

<212>   PRT

<213>   homo sapien

<220>

-7-

<221> MISC_FEATURE

<222> (43)..(43)

<223> unknown amino acid

<220>

<221> MISC_FEATURE

<222> (192)..(192)

<223> unknown amino acid

<220>

<221> MISC_FEATURE

<222> (255)..(255)

<223> unknown amino acid

<220>

<221> MISC_FEATURE

<222> (258)..(258)

<223> unknown amino acid

<220>

<221> MISC_FEATURE

<222> (374)..(374)

<223> unknown amino acid

<220>

<221> MISC_FEATURE

<222> (397)..(397)

<223> unknown amino acid

<220>

<221> MISC_FEATURE

<222> (452)..(452)

<223> unknown amino acid

<220>

<221> MISC_FEATURE

<222> (458)..(458)

<223> unknown amino acid

<220>

<221> MISC_FEATURE

<222> (475)..(475)

<223> unknown amino acid

<220>

<221> MISC_FEATURE

<222> (487)..(487)

<223> unknown amino acid

<400> 6

Ser Phe Gly Leu Glu His Asp Gly Ala Pro Gly Ser Gly Cys Gly Pro
1   5   10   15

Ser Gly His Val Met Ala Ser Glu Arg Arg Arg Pro Ala Pro Ala Ser
            20   25   30

Pro Gly Pro Pro Ala Ala Ala Gly Ser Cys Xaa Ala Cys Ser Asp Pro
        35   40   45

Ser Leu Arg Arg Arg Ser Leu Cys Trp Pro Pro Thr Ser Ala Pro Ala
    50   55   60

Gly Ala Leu Val Leu Val Pro Ala Lys Ser Arg Leu Leu Val Gly Gly
65   70   75   80

Ala Gly Arg Glu Leu Leu Phe Pro Leu Thr Lys Gly His Ala Ser Lys
                    85   90   95

Arg Phe His Pro Arg Ala His Ser Ser Val Pro Pro Pro Pro Gly Val
                    100   105   110

His Pro Gly Thr Glu Pro Gly Leu Ser Arg Ala Leu Ser Gln Arg Met
                    115   120   125

Thr Gly Ala Leu Val Trp Asp Pro Pro Arg Pro Gln Pro Gly Ser Ala
        130   135   140

Gly His Pro Arg Asn Ala His Leu Gly Leu Tyr Tyr Ser Ala Asn Glu
145   150   155   160

Gln Cys Arg Val Ala Phe Gly Pro Lys Ala Val Ala Cys Thr Phe Ala
                    165   170   175

Arg Glu His Leu Val Ser Leu Pro Ala Val Ala Trp Asp Trp Leu Xaa
                180   185   190

Gly Pro Ser Ala Ser Pro Ser Ser Arg Pro Pro Lys Arg Ala Trp Ile
            195   200   205

Cys Ala Arg Pro Ser Pro Ala Thr Gln Thr Arg Trp Thr Lys Ala Ala
    210   215   220

Ala Ala Ala Ser Ser Phe Leu Ser Trp Met Gly Gln Asn Val Ala Trp
225   230   235   240

Arg Ser Gly Ala Pro Arg Val Ala Ala Ala Pro Trp Trp Ser Xaa Pro
                245   250   255

Pro Xaa Gln Gln Cys Met Gly Ala Gly Leu Ala Gly Val Pro Glu Val
            260   265   270

Leu Ala Pro Ala Pro Ala Glu Glu Val Trp Ser Pro Gly Gly Gly Ser
        275   280   285

Ala Thr Thr Pro Asp Leu Pro Leu Gly Gly Val His Val Leu Val Leu
        290   295   300

Thr Ser Arg Pro Arg Cys Ala Thr Leu Arg Pro Ala Arg Arg Pro Ser
305   310   315   320

-10-

```
Trp Ser Ser Cys Arg Asn Ser Ala Pro Gly Pro Thr Ala Ser Arg Cys
            325             330             335

Ala Pro Pro Leu Ala Ala Pro Pro Ser Thr Thr Gly Val Leu Leu Tyr
            340             345             350

His Thr Ala Lys Gly Met Leu Cys Ala Asp Thr Cys Ala Gly Pro Leu
            355             360             365

Ala Arg Ala Ser Ser Xaa Ser Val Glu Thr Ala Ser Ser Met Gly Pro
    370             375             380

Gly Val Cys Gln Val Ala Pro Gly Arg Thr Gly Pro Xaa Ala Cys Val
385             390             395             400

Cys Arg Ala Ala Ala Gly His Leu Ala Val Met Val Gly Trp Thr Pro
            405             410             415

Ser Arg Tyr Gly Thr Gly Ala Arg Cys Val Val Gly Thr Thr Ala Arg
            420             425             430

Ala Ala His Gly Arg Ala Leu Ser Gln Leu Ala Glu Arg Glu Asn Met
            435             440             445

Ser Arg Phe Xaa Gln Leu Pro Pro Thr Xaa Pro Val Ser Thr Leu Pro
    450             455             460

Thr Thr Gly Leu Ser Ser His Thr Trp Arg Xaa Gly Ser Glu Gly Ala
465             470             475             480

Met Ser Trp Leu Gly Arg Xaa Ala Ser Pro Leu Thr Pro Pro Thr Pro
            485             490             495

Pro Ser Trp Arg Met Val Val Ser Ser Thr Glu Trp Pro Ser Pro Arg
            500             505             510

Thr Gly Cys Pro Ala Trp Arg Arg Ser Ala Ser Gly Asp Pro Ser Arg
            515             520             525

Lys Met Leu Thr Ser Arg Trp Glu Val Ser Glu Pro Ser Ser Cys Thr
            530             535             540

Ser Ala Gly Gly Ala Gly Leu Ala Leu Glu Asn Glu Thr Cys Val Pro
545             550             555             560
```

Gly Ala Asp Gly Leu Glu Ala Pro Val Thr Glu Gly Pro Gly Ser Val
565   570   575

Asp Glu Lys Leu Pro Ala Pro Glu Pro Cys Val Gly Met Ser Cys Pro
580   585   590

Pro Gly Trp Gly His Leu Asp Ala Thr Ser Ala Gly Glu Lys Ala Pro
595   600   605

Ser Pro Trp Gly Ser Ile Arg Thr Gly Ala Gln Ala Ala His Val Trp
610   615   620

Thr Pro Ala Ala Gly Ser Cys Ser Val Ser Cys Gly Arg Gly Leu Met
625   630   635   640

Glu Leu Arg Phe Leu Cys Met Asp Ser Ala Leu Arg Val Pro Val Gln
645   650   655

Glu Glu Leu Cys Gly Leu Ala Ser Lys Pro Gly Ser Arg Arg Glu Val
660   665   670

Cys Gln Ala Val Pro Cys Pro Ala Arg Trp Gln Tyr Lys Leu Ala Ala
675   680   685

Cys Ser Val Ser Cys Gly Arg Gly Val Val Arg Arg Ile Leu Tyr Cys
690   695   700

Ala Arg Ala His Gly Glu Asp Asp Gly Glu Glu Ile Leu Leu Asp Thr
705   710   715   720

Gln Cys Gln Gly Leu Pro Arg Pro Glu Pro Gln Glu Ala Cys Ser Leu
725   730   735

Glu Pro

<210>   7

<211>   4284

<212>   DNA

<213>   homo sapien

<400>   7

-12-

```
atgcaccagc gtcacccctg ggcaagatgc cctcccctct gtgtggccgg aatccttgcc      60

tgtggctttc tcctgggctg ctggggaccc tcccatttcc agcagagttg tcttcaggct     120

ttggagccac aggccgtgtc ttcttacttg agccctggtg ctcccttaaa aggccgccct     180

ccttcccctg gcttccagag gcagaggcag aggcagaggc gggctgcagg cggcatccta     240

cacctggagc tgctggtggc cgtgggcccc gatgtcttcc aggctcacca ggaggacaca     300

gagcgctatg tgctcaccaa cctcaacatc ggggcagaac tgcttcggga cccgtccctg     360

ggggctcagt ttcgggtgca cctggtgaag atggtcattc tgacagagcc tgagggtgcc     420

ccaaatatca cagccaacct cacctcgtcc ctgctgagcg tctgtgggtg gagccagacc     480

atcaaccctg aggacgacac ggatcctggc catgctgacc tggtcctcta tatcactagg     540

tttgacctgg agttgcctga tggtaaccgg caggtgcggg gcgtcaccca gctgggcggt     600

gcctgctccc caacctggag ctgcctcatt accgaggaca ctggcttcga cctgggagtc     660

accattgccc atgagattgg gcacagcttc ggcctggagc acgacggcgc gcccggcagc     720

ggctgcggcc ccagcggaca cgtgatggct tcggacggcg ccgcgccccg cgccggcctc     780

gcctggtccc cctgcagccg ccggcagctg ctgagcctgc tcagcgcagg acgggcgcgc     840

tgcgtgtggg acccgccgcg gcctcaaccc gggtccgcgg ggcacccgcc ggatgcgcag     900

cctggcctct actacagcgc caacgagcag tgccgcgtgg ccttcggccc caaggctgtc     960

gcctgcacct tcgccaggga gcacctggat atgtgccagg ccctctcctg ccacacagac    1020

ccgctggacc aaagcagctg cagccgcctc ctcgttcctc tcctggatgg gacagaatgt    1080

ggcgtggaga agtggtgctc caagggtcgc tgccgctccc tggtggagct gacccccata    1140

gcagcagtgc atgggcgctg gtctagctgg ggtccccgaa gtccttgctc cgctcctgc     1200

ggaggaggtg tggtcaccag gaggcggcag tgcaacaacc cagacctgc ctttgggggg     1260

cgtgcatgtg ttggtgctga cctccaggcc gagatgtgca cactcaggc ctgcgagaag    1320

acccagctgg agttcatgtc gcaacagtgc gccaggaccg acggccagcc gctgcgctcc    1380

tcccctggcg gcgcctcctt ctaccactgg ggtgctgctg taccacacag ccaaggggat    1440

gctctgtgca gacacatgtg ccgggccatt ggcgagagct tcatcatgaa gcgtggagac    1500

agcttcctcg atgggacccg gtgtatgcca agtggccccc gggaggacgg gaccctgagc    1560

ctgtgtgtgt cggcagctg caggacattt ggctgtgatg gtaggatgga ctcccagcag    1620

gtatgggaca ggtgccaggt gtgtggtggg gacaacagca cgtgcagccc acggaagggc    1680

tctttcacag ctggcagagc gagagaatat gtcacgtttc tgacagttac ccccaacctg    1740

accagtgtct acattgccaa ccacaggcct ctcttcacac acttggcggt gaggatcgga    1800
```

```
gggcgctatg tcgtggctgg gaagatgagc atctcccta acaccaccta cccctccctc      1860

ctggaggatg gtcgtgtcga gtacagagtg gccctcaccg aggaccggct gccccgcctg      1920

gaggagatcc gcatctgggg acccctccag gaagatgctg acatccaggt ttacaggcgg      1980

tatggcgagg agtatggcaa cctcacccgc ccagacatca ccttcaccta cttccagcct      2040

aagccacggc aggcctgggt gtgggccgct gtgcgtgggc cctgctcggt gagctgtggg      2100

gcagggctgc gctgggtaaa ctacagctgc ctggaccagg ccaggaagga gttggtggag      2160

actgtccagt gccaagggag ccagcagcca ccagcgtggc cagaggcctg cgtgctcgaa      2220

ccctgccctc cctactgggc ggtgggagac ttcggcccat gcagcgcctc ctgtggggc      2280

ggcctgcggg agcggccagt gcgctgcgtg gaggcccagg gcagcctcct gaagacattg      2340

cccccagccc ggtgcagagc aggggcccag cagccagctg tggcgctgga aacctgcaac      2400

ccccagccct gccctgccag gtgggaggtg tcagagccca gctcatgcac atcagctggt      2460

ggagcaggcc tggccttgga gaacgagacc tgtgtgccag gggcagatgg cctggaggct      2520

ccagtgactg aggggcctgg ctccgtagat gagaagctgc ctgcccctga gccctgtgtc      2580

gggatgtcat gtcctccagg ctggggccat ctggatgcca cctctgcagg ggagaaggct      2640

ccctccccat ggggcagcat caggacgggg gctcaagctg cacacgtgtg dacccctgcg      2700

gcagggtcgt gctccgtctc ctgcgggcga ggtctgatgg agctgcgttt cctgtgcatg      2760

gactctgccc tcagggtgcc tgtccaggaa gagctgtgtg cctggcaag caagcctggg      2820

agccggcggg aggtctgcca ggctgtcccg tgccctgctc ggtggcagta caagctggcg      2880

gcctgcagcg tgagctgtgg gagaggggtc gtgcggagga tcctgtattg tgcccgggcc      2940

catggggagg acgatggtga ggagatcctg ttggacaccc agtgccaggg gctgcctcgc      3000

ccggaacccc aggaggcctg cagcctggag ccctgcccac ctaggtggaa agtcatgtcc      3060

cttggcccat gttcggccag ctgtggcctt ggcactgcta gacgctcggt ggcctgtgtg      3120

cagctcgacc aaggccagga cgtggaggtg gacgaggcgg cctgtgcggc gctggtgcgg      3180

cccgaggcca gtgtcccctg tctcattgcc gactgcacct accgctggca tgttggcacc      3240

tggatggagt gctctgtttc ctgtgggggat ggcatccagc gccggcgtga cacctgcctc      3300

ggaccccagg cccagcgcc tgtgccagct gatttctgcc agcacttgcc caagccggtg      3360

actgtgcgtg gctgctgggc tgggccctgt gtgggacagg gtacgcccag cctggtgccc      3420

cacgaagaag ccgctgctcc aggacggacc acagccaccc tgctggtgc ctccctggag      3480

tggtcccagg cccgggggcct gctcttctcc ccggctcccc agcctcggcg gctcctgccc      3540

gggccccagg aaaactcagt gcagtccagt gcctgtggca ggcagcacct tgagccaaca      3600
```

-14-

ggaaccattg acatgcgagg cccagggcag gcagactgtg cagtggccat tgggcggccc   3660

ctcggggagg tggtgaccct ccgcgtcctt gagagttctc tcaactgcag tgcggggggac   3720

atgttgctgc tttggggccg gctcacctgg aggaagatgt gcaggaagct gttggacatg   3780

actttcagct ccaagaccaa cacgctggtg gtgaggcagc gctgcgggcg gccaggaggt   3840

ggggtgctgc tgcggtatgg gagccagctt gctcctgaaa ccttctacag agaatgtgac   3900

atgcagctct ttgggccctg gggtgaaatc gtgagcccct cgctgagtcc agccacgagt   3960

aatgcagggg gctgccggct cttcattaat gtggctccgc acgcacggat tgccatccat   4020

gccctggcca ccaacatggg cgctgggacc gagggagcca atgccagcta catcttgatc   4080

cgggacaccc acagcttgag gaccacagcg ttccatgggc agcaggtgct ctactgggag   4140

tcagagagca gccaggctga gatggagttc agcgagggct tcctgaaggc tcaggccagc   4200

ctgcgggggcc agtactggac cctccaatca tgggtaccgg agatgcagga ccctcagtcc   4260

tggaagggaa aggaaggaac ctga   4284

<210>   8

<211>   1427

<212>   PRT

<213>   homo sapiens

<400>   8

Met His Gln Arg His Pro Trp Ala Arg Cys Pro Pro Leu Cys Val Ala
1   5   10   15

Gly Ile Leu Ala Cys Gly Phe Leu Leu Gly Cys Trp Gly Pro Ser His
            20   25   30

Phe Gln Gln Ser Cys Leu Gln Ala Leu Glu Pro Gln Ala Val Ser Ser
        35   40   45

Tyr Leu Ser Pro Gly Ala Pro Leu Lys Gly Arg Pro Pro Ser Pro Gly
    50   55   60

Phe Gln Arg Gln Arg Gln Arg Gln Arg Arg Ala Ala Gly Gly Ile Leu
65   70   75   80

His Leu Glu Leu Leu Val Ala Val Gly Pro Asp Val Phe Gln Ala His
                85   90   95

-15-

Gln Glu Asp Thr Glu Arg Tyr Val Leu Thr Asn Leu Asn Ile Gly Ala
            100   105   110

Glu Leu Leu Arg Asp Pro Ser Leu Gly Ala Gln Phe Arg Val His Leu
            115   120   125

Val Lys Met Val Ile Leu Thr Glu Pro Glu Gly Ala Pro Asn Ile Thr
        130   135   140

Ala Asn Leu Thr Ser Ser Leu Leu Ser Val Cys Gly Trp Ser Gln Thr
145   150   155   160

Ile Asn Pro Glu Asp Asp Thr Asp Pro Gly His Ala Asp Leu Val Leu
                165   170   175

Tyr Ile Thr Arg Phe Asp Leu Glu Leu Pro Asp Gly Asn Arg Gln Val
                180   185   190

Arg Gly Val Thr Gln Leu Gly Gly Ala Cys Ser Pro Thr Trp Ser Cys
        195   200   205

Leu Ile Thr Glu Asp Thr Gly Phe Asp Leu Gly Val Thr Ile Ala His
        210   215   220

Glu Ile Gly His Ser Phe Gly Leu Glu His Asp Gly Ala Pro Gly Ser
225   230   235   240

Gly Cys Gly Pro Ser Gly His Val Met Ala Ser Asp Gly Ala Ala Pro
                245   250   255

Arg Ala Gly Leu Ala Trp Ser Pro Cys Ser Arg Arg Gln Leu Leu Ser
            260   265   270

Leu Leu Ser Ala Gly Arg Ala Arg Cys Val Trp Asp Pro Pro Arg Pro
        275   280   285

Gln Pro Gly Ser Ala Gly His Pro Pro Asp Ala Gln Pro Gly Leu Tyr
    290   295   300

Tyr Ser Ala Asn Glu Gln Cys Arg Val Ala Phe Gly Pro Lys Ala Val
305   310   315   320

Ala Cys Thr Phe Ala Arg Glu His Leu Asp Met Cys Gln Ala Leu Ser
                325   330   335

-16-

```
Cys His Thr Asp Pro Leu Asp Gln Ser Ser Cys Ser Arg Leu Leu Val
        340                 345                 350

Pro Leu Leu Asp Gly Thr Glu Cys Gly Val Glu Lys Trp Cys Ser Lys
        355                 360                 365

Gly Arg Cys Arg Ser Leu Val Glu Leu Thr Pro Ile Ala Ala Val His
        370                 375                 380

Gly Arg Trp Ser Ser Trp Gly Pro Arg Ser Pro Cys Ser Arg Ser Cys
385                 390                 395                 400

Gly Gly Gly Val Val Thr Arg Arg Arg Gln Cys Asn Asn Pro Arg Pro
                405                 410                 415

Ala Phe Gly Gly Arg Ala Cys Val Gly Ala Asp Leu Gln Ala Glu Met
        420                 425                 430

Cys Asn Thr Gln Ala Cys Glu Lys Thr Gln Leu Glu Phe Met Ser Gln
        435                 440                 445

Gln Cys Ala Arg Thr Asp Gly Gln Pro Leu Arg Ser Ser Pro Gly Gly
        450                 455                 460

Ala Ser Phe Tyr His Trp Gly Ala Ala Val Pro His Ser Gln Gly Asp
465                 470                 475                 480

Ala Leu Cys Arg His Met Cys Arg Ala Ile Gly Glu Ser Phe Ile Met
                485                 490                 495

Lys Arg Gly Asp Ser Phe Leu Asp Gly Thr Arg Cys Met Pro Ser Gly
        500                 505                 510

Pro Arg Glu Asp Gly Thr Leu Ser Leu Cys Val Ser Gly Ser Cys Arg
        515                 520                 525

Thr Phe Gly Cys Asp Gly Arg Met Asp Ser Gln Gln Val Trp Asp Arg
        530                 535                 540

Cys Gln Val Cys Gly Gly Asp Asn Ser Thr Cys Ser Pro Arg Lys Gly
545                 550                 555                 560

Ser Phe Thr Ala Gly Arg Ala Arg Glu Tyr Val Thr Phe Leu Thr Val
                565                 570                 575
```

-17-

Thr Pro Asn Leu Thr Ser Val Tyr Ile Ala Asn His Arg Pro Leu Phe
            580   585   590

Thr His Leu Ala Val Arg Ile Gly Gly Arg Tyr Val Val Ala Gly Lys
        595   600   605

Met Ser Ile Ser Pro Asn Thr Thr Tyr Pro Ser Leu Leu Glu Asp Gly
        610   615   620

Arg Val Glu Tyr Arg Val Ala Leu Thr Glu Asp Arg Leu Pro Arg Leu
625   630   635   640

Glu Glu Ile Arg Ile Trp Gly Pro Leu Gln Glu Asp Ala Asp Ile Gln
                645   650   655

Val Tyr Arg Arg Tyr Gly Glu Glu Tyr Gly Asn Leu Thr Arg Pro Asp
                660   665   670

Ile Thr Phe Thr Tyr Phe Gln Pro Lys Pro Arg Gln Ala Trp Val Trp
            675   680   685

Ala Ala Val Arg Gly Pro Cys Ser Val Ser Cys Gly Ala Gly Leu Arg
        690   695   700

Trp Val Asn Tyr Ser Cys Leu Asp Gln Ala Arg Lys Glu Leu Val Glu
705   710   715   720

Thr Val Gln Cys Gln Gly Ser Gln Gln Pro Pro Ala Trp Pro Glu Ala
                725   730   735

Cys Val Leu Glu Pro Cys Pro Pro Tyr Trp Ala Val Gly Asp Phe Gly
            740   745   750

Pro Cys Ser Ala Ser Cys Gly Gly Gly Leu Arg Glu Arg Pro Val Arg
        755   760   765

Cys Val Glu Ala Gln Gly Ser Leu Leu Lys Thr Leu Pro Pro Ala Arg
        770   775   780

Cys Arg Ala Gly Ala Gln Gln Pro Ala Val Ala Leu Glu Thr Cys Asn
785   790   795   800

Pro Gln Pro Cys Pro Ala Arg Trp Glu Val Ser Glu Pro Ser Ser Cys
            805   810   815

-18-

```
Thr Ser Ala Gly Gly Ala Gly Leu Ala Leu Glu Asn Glu Thr Cys Val
        820             825             830

Pro Gly Ala Asp Gly Leu Glu Ala Pro Val Thr Glu Gly Pro Gly Ser
        835             840             845

Val Asp Glu Lys Leu Pro Ala Pro Glu Pro Cys Val Gly Met Ser Cys
    850             855             860

Pro Pro Gly Trp Gly His Leu Asp Ala Thr Ser Ala Gly Glu Lys Ala
865             870             875             880

Pro Ser Pro Trp Gly Ser Ile Arg Thr Gly Ala Gln Ala Ala His Val
            885             890             895

Trp Thr Pro Ala Ala Gly Ser Cys Ser Val Ser Cys Gly Arg Gly Leu
        900             905             910

Met Glu Leu Arg Phe Leu Cys Met Asp Ser Ala Leu Arg Val Pro Val
        915             920             925

Gln Glu Glu Leu Cys Gly Leu Ala Ser Lys Pro Gly Ser Arg Arg Glu
    930             935             940

Val Cys Gln Ala Val Pro Cys Pro Ala Arg Trp Gln Tyr Lys Leu Ala
945             950             955             960

Ala Cys Ser Val Ser Cys Gly Arg Gly Val Val Arg Arg Ile Leu Tyr
            965             970             975

Cys Ala Arg Ala His Gly Glu Asp Asp Gly Glu Glu Ile Leu Leu Asp
        980             985             990

Thr Gln Cys Gln Gly Leu Pro Arg  Pro Glu Pro Gln Glu  Ala Cys Ser
        995             1000             1005

Leu Glu  Pro Cys Pro Pro Arg  Trp Lys Val Met Ser  Leu Gly Pro
    1010             1015             1020

Cys Ser  Ala Ser Cys Gly Leu  Gly Thr Ala Arg Arg  Ser Val Ala
    1025             1030             1035

Cys Val  Gln Leu Asp Gln Gly  Gln Asp Val Glu Val  Asp Glu Ala
    1040             1045             1050
```

```
Ala Cys  Ala Ala Leu Val Arg  Pro Glu Ala Ser Val  Pro Cys Leu
    1055                 1060                 1065


Ile Ala  Asp Cys Thr Tyr Arg  Trp His Val Gly Thr  Trp Met Glu
    1070                 1075                 1080


Cys Ser  Val Ser Cys Gly Asp  Gly Ile Gln Arg Arg  Arg Asp Thr
    1085                 1090                 1095


Cys Leu  Gly Pro Gln Ala Gln  Ala Pro Val Pro Ala  Asp Phe Cys
    1100                 1105                 1110


Gln His  Leu Pro Lys Pro Val  Thr Val Arg Gly Cys  Trp Ala Gly
    1115                 1120                 1125


Pro Cys  Val Gly Gln Gly Thr  Pro Ser Leu Val Pro  His Glu Glu
    1130                 1135                 1140


Ala Ala  Ala Pro Gly Arg Thr  Thr Ala Thr Pro Ala  Gly Ala Ser
    1145                 1150                 1155


Leu Glu  Trp Ser Gln Ala Arg  Gly Leu Leu Phe Ser  Pro Ala Pro
    1160                 1165                 1170


Gln Pro  Arg Arg Leu Leu Pro  Gly Pro Gln Glu Asn  Ser Val Gln
    1175                 1180                 1185


Ser Ser  Ala Cys Gly Arg Gln  His Leu Glu Pro Thr  Gly Thr Ile
    1190                 1195                 1200


Asp Met  Arg Gly Pro Gly Gln  Ala Asp Cys Ala Val  Ala Ile Gly
    1205                 1210                 1215


Arg Pro  Leu Gly Glu Val Val  Thr Leu Arg Val Leu  Glu Ser Ser
    1220                 1225                 1230


Leu Asn  Cys Ser Ala Gly Asp  Met Leu Leu Leu Trp  Gly Arg Leu
    1235                 1240                 1245


Thr Trp  Arg Lys Met Cys Arg  Lys Leu Leu Asp Met  Thr Phe Ser
    1250                 1255                 1260


Ser Lys  Thr Asn Thr Leu Val  Val Arg Gln Arg Cys  Gly Arg Pro
    1265                 1270                 1275
```

```
Gly Gly  Gly Val Leu Leu Arg  Tyr Gly Ser Gln Leu  Ala Pro Glu
    1280                1285                1290


Thr Phe  Tyr Arg Glu Cys Asp  Met Gln Leu Phe Gly  Pro Trp Gly
    1295                1300                1305


Glu Ile  Val Ser Pro Ser Leu  Ser Pro Ala Thr Ser  Asn Ala Gly
    1310                1315                1320


Gly Cys  Arg Leu Phe Ile Asn  Val Ala Pro His Ala  Arg Ile Ala
    1325                1330                1335


Ile His  Ala Leu Ala Thr Asn  Met Gly Ala Gly Thr  Glu Gly Ala
    1340                1345                1350


Asn Ala  Ser Tyr Ile Leu Ile  Arg Asp Thr His Ser  Leu Arg Thr
    1355                1360                1365


Thr Ala  Phe His Gly Gln Gln  Val Leu Tyr Trp Glu  Ser Glu Ser
    1370                1375                1380


Ser Gln  Ala Glu Met Glu Phe  Ser Glu Gly Phe Leu  Lys Ala Gln
    1385                1390                1395


Ala Ser  Leu Arg Gly Gln Tyr  Trp Thr Leu Gln Ser  Trp Val Pro
    1400                1405                1410


Glu Met  Gln Asp Pro Gln Ser  Trp Lys Gly Lys Glu  Gly Thr
    1415                1420                1425
```